

SEQUENCE LISTING



6.

<110> Agarwal, Poonam
Aizenstein, Brian
Arco, David
Atilas, Myrta
Burris, Deborah
de Arruda Indig, Monika
Law, Scott
Mast, Andrea
Marshall, David
Miller, Carolyn
Oldenberg, Mary
Rasmussen, Eric
Schneiders, Jennifer

<120> Methods and Compositions for Detecting Target Sequences
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Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
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Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65 70 75 80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
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Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
100 105 110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
115 120 125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
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145 150 155 160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175
Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
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Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
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Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
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Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
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Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
245 250 255
Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
260 265 270
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
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Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
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Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
305 310 315 320

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 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
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 385 390 395 400
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 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
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 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
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 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
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 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
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 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
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 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
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 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
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 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
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 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
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 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 785 790 795 800
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 35 40 45
 Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
 50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
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 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
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 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
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 Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
 165 170 175
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
 210 215 220
 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
 225 230 235 240
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
 260 265 270
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
 275 280 285
 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 290 295 300
 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
 305 310 315 320
 Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp
 325 330 335
 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala
 340 345 350
 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
 355 360 365
 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
 405 410 415

Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
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 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
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 Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
 500 505 510
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525
 Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540
 Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His
 545 550 555 560
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 565 570 575
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 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
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 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
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 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
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 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
 675 680 685
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
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Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
770 775 780

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785 790 795 800

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Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
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Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	
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 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
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 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
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 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
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 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
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 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
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 690 695 700
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Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
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Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
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Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
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 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
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 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
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 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
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 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
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 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
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 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
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 <220>
 <223> Synthetic
 <400> 36
 cctttcgctt tcttccttc ctttctcgcc acgttcgccg gc 42
 <210> 37
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 37
 cctttcgctc tcttccttc ctttctcgcc acgttcgccg gc 42
 <210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (8)..(8)
 <223> The residue at this position is 2'-O-methyladenosine.
 <400> 38
 agaaaggaag ggaagaaagc gaaaggt 27

<210>	39	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	39	
	gccggcgaac gtggcgagaa agga	24
<210>	40	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	40	
	ggtttttctt tgaggtttag	20
<210>	41	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	41	
	gcgacactcc accatagat	19
<210>	42	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	42	
	ctgtcttcac gcagaaagc	19

<210> 43
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 43
 gcacggtcta cgagacctc 19
 <210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 44
 taatacgact cactataggg 20
 <210> 45
 <211> 337
 <212> RNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 45
 gggaaagcuu gcaugccugc agguccgacuc uagaggaucau acuaugacua uggauucugu 60
 cuucacgcag aaagcgucug gccauggcgu uaguaugagu gucgugcagc cuccaggacc 120
 cccccucccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aaaugccagg 180
 acgaccgggu ccuuucuugg auaaaccgcg ucaaugccug gagauuuggg cgugcccccg 240
 caagacugcu agccgaguag uguugggucg cgaaaggccu ugugguacug ccugauaggg 300
 ugccugcgag ugccccggga ggucucguag accgugc 337
 <210> 46
 <211> 19
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (17)..(17)
 <223> The T at this position is linked to a fluorescein dye on an abasic linker
 <400> 46
 ccggtcgtcc tggcaatcc 19
 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 47
 gtttatccaa gaaaggaccc ggtc 24
 <210> 48
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 48
 cagggtgaag ggaagaagaa agcgaaaggt 30
 <210> 49
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 49
 cagggggaag ggaagaagaa agcgaaaggt 30

<210> 50
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The T residues at these positions are amino modified T residues.
 <400> 50
 ttcttttcac cagcgagacg gg 22
 <210> 51
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 51
 attgggcgcc aggggtggttt tt 22
 <210> 52
 <211> 53
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 52
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210>	53	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	53	
	gaattcgatt taggtgacac tatagaatac a	31
<210>	54	
<211>	42	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	54	
	cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc	42
<210>	55	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	55	
	gccggcgaac gtggcgagaa agga	24
<210>	56	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	56	
	cagaaggaag ggaagaaagc gaaagg	26

<210> 57	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 57	
cagggggaag ggaagaaagc gaaagg	26
<210> 58	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 58	
caggggtacag ggaagaaagc gaaagg	26
<210> 59	
<211> 42	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 59	
gggaaagtcc tcggagccgc gcgggacgag cgtggggggcc cg	42
<210> 60	
<211> 963	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<220>	

<221> CDS

<222> (1)..(960)

<400> 60

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Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly	
1 5 10 15	
atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc	96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly	
20 25 30	
cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc	144
His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr	
35 40 45	
agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc	192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu	
50 55 60	
ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac	240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp	
65 70 75 80	
gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg	288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala	
85 90 95	
ggc cgg gcc ccc acg ctc gtc ccg cgc ggc tcc gag gac ttt ccc cgg	336
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg	
100 105 110	
caa ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc	384
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg	
115 120 125	
ctc gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc	432
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala	
130 135 140	
aag aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac	480
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	
145 150 155 160	
aaa gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc	528
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	
165 170 175	
gag ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg	576
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	
180 185 190	
agg ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc	624
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	
195 200 205	
gac aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag	672
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys	
210 215 220	

ctt	ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	720
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	
225					230					235					240	
cgg	ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	768
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	
				245					250					255		
ctg	aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	816
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	
			260					265					270			
gag	gtg	gac	ttc	gcc	aaa	agg	cgg	gag	ccc	gac	cgg	gag	agg	ctt	agg	864
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	
		275					280					285				
gcc	ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc	912
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	
	290					295					300					
ctt	ctg	gaa	agc	ccc	aag	gcc	gca	ctc	gag	cac	cac	cac	cac	cac	cac	960
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Ala	Leu	Glu	His	His	His	His	His	His	
305					310					315					320	
tga																963

<210> 61

<211> 320

<212> PRT

<213> Artificial Sequence

<400> 61

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser	Gly
1				5					10					15	

Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
			20					25					30		

His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		35					40					45			

Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
	50					55					60				

Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
65					70					75					80

Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	Lys	Ala
				85					90					95	

Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg
 100 105 110

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg
 115 120 125

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala
 130 135 140

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 145 150 155 160

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
 165 170 175

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
 180 185 190

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
 195 200 205

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys
 210 215 220

Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 225 230 235 240

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 245 250 255

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 260 265 270

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 275 280 285

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 290 295 300

Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His
 305 310 315 320

<210> 62

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 62

cgatctcctc ggccacctcc

20

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 63

ggcggtgccc tggacgggca

20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 64

ccagctcggt gtggacctga

20

<210> 65

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1) .. (2499)

<400> 65

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu	
1 5 10 15	
ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag	96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	
20 25 30	
ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc	144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	
35 40 45	
gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc	192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	
50 55 60	
gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg	240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	
65 70 75 80	
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa	288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	
85 90 95	
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc	336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	
100 105 110	
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	

ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg	1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	
450 455 460	

gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565 570 575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112

cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 66

<211> 833

<212> PRT

<213> Artificial Sequence

<400> 66

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

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<210> 68

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48

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

96

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

144

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

192

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly 65 70 75 80	240
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln 85 90 95	288
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu 100 105 110	336
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys 115 120 125	384
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys 130 135 140	432
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag Asp Leu Tyr Gln Leu Ser Asp Arg Ile His Val Leu His Pro Glu 145 150 155 160	480
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175	528
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190	576
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205	624
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220	672
ctg aag ccc gcc atc ccg gag aag atc ctg gcc cac atg gac gat ctg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240	720
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255	768
gtg gac ttc gcc aaa agg ccg gag ccc gac ccg gag agg ctt agg gcc Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270	816
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285	864
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300	912

ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320	960
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Arg Gly Arg Val His Arg Ala 325 330 335	1008
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350	1056
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365	1104
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380	1152
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400	1200
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 415	1248
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430	1296
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445	1344
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460	1392
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584

atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
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cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
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acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr 705 710 715 720	2160
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 735	2208
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750	2256
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765	2304

ctc	ttc	ccc	agg	ctg	gag	gaa	atg	ggg	gcc	agg	atg	ctc	ctt	cag	gtc	2352
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
	770					775					780					

cac	gac	gag	ctg	gtc	ctc	gag	gcc	cca	aaa	gag	agg	gcg	gag	gcc	gtg	2400
His	Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	
	785				790					795					800	

gcc	cgg	ctg	gcc	aag	gag	gtc	atg	gag	ggg	gtg	tat	ccc	ctg	gcc	gtg	2448
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
				805					810					815		

ccc	ctg	gag	gtg	gag	gtg	ggg	ata	ggg	gag	gac	tgg	ctc	tcc	gcc	aag	2496
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
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Glu																

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<213> Artificial Sequence

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Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
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Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				

Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80

Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
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Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		

Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
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Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
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 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
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 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
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 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
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 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
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 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
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 Glu

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ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag      96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
          20          25          30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc      144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
          35          40          45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc      192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
          50          55          60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65          70          75          80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
          85          90          95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
          100          105          110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
          115          120          125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
          130          135          140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145          150          155          160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
          165          170          175

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Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	

420								425				430								
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Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr					
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ggg	gtg	cgc	ctg	gac	gtg	gcc	tat	ctc	agg	gcc	ttg	tcc	ctg	gag	gtg	1392				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val					
	450					455					460									
gcc	ggg	gag	atc	gcc	cgc	ctc	gag	gcc	gag	gtc	ttc	cgc	ctg	gcc	ggc	1440				
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly					
465					470					475					480					
cac	ccc	ttc	aac	ctc	aac	tcc	cgg	gac	cag	ctg	gaa	agg	gtc	ctc	ttt	1488				
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe					
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gac	gag	cta	ggg	ctt	ccc	gcc	atc	ggc	aag	acg	gag	aag	acc	ggc	aag	1536				
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys					
			500					505					510							
cgc	tcc	acc	agc	gcc	gcc	gtc	ctg	gag	gcc	ctc	cgc	gag	gcc	cac	ccc	1584				
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro					
		515				520						525								
atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser					
	530					535					540									
acc	tac	att	gac	ccc	ttg	ccg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg					
545					550					555					560					
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728				
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser					
				565				570						575						
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776				
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly					
			580					585					590							
cag	agg	atc	cgc	cgg	gcc	ttc	atc	gcc	gag	gag	ggg	tgg	cta	ttg	gtg	1824				
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val					
		595				600						605								
gcc	ctg	gtc	tat	agc	cag	ata	gag	ctc	agg	gtg	ctg	gcc	cac	ctc	tcc	1872				
Ala	Leu	Val	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser					
	610					615					620									
ggc	gac	gag	aac	ctg	atc	cgg	gtc	ttc	cag	gag	ggg	cgg	gac	atc	cac	1920				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His					
625					630					635					640					
acg	gag	acc	gcc	agc	tgg	atg	ttc	ggc	gtc	ccc	cgg	gag	gcc	gtg	gac	1968				
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp					
			645					650						655						
ccc	ctg	atg	cgc	cgg	gcg	gcc	aag	acc	atc	aac	ttc	ggg	gtc	ctc	tac	2016				
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr					
			660					665					670							

ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag	2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu	
675 680 685	
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg	2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	
690 695 700	
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 71

<211> 833

<212> PRT

<213> Artificial Sequence

<400> 71

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Glu

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 72
 gggataccat gggagtgcag tttgg

25

<210> 73

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73
 ggtaaatttt tctcgtcgac atcccac

27

<210> 74

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1) .. (978)

<400> 74

atg gga gtg cag ttt ggt gat ttt att cca aaa aat att atc tcc ttt	48
Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe	
1 5 10 15	
gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta	96
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu	
20 25 30	
tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga	144
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg	
35 40 45	
aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa	192
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys	
50 55 60	
acc ata cat ttg tta gag aat gat ata act cca atc tgg gtt ttt gat	240
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp	
65 70 75 80	
ggg gag cca cca aag tta aag gag aaa aca agg aaa gtt agg aga gag	288
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu	
85 90 95	
atg aaa gag aaa gct gaa ctt aag atg aaa gag gca att aaa aag gag	336
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu	
100 105 110	
gat ttt gaa gaa gct gct aag tat gca aag agg gtt agc tat cta act	384
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr	
115 120 125	
ccg aaa atg gtt gaa aac tgc aaa tat ttg tta agt ttg atg ggc att	432
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile	
130 135 140	
ccg tat gtt gaa gct ccc tct gag gga gag gca caa gca agc tat atg	480
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met	
145 150 155 160	
gca aag aag gga gat gtt tgg gca gtt gta agt caa gat tat gat gcc	528
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala	
165 170 175	
ttg tta tat gga gct ccg aga gtt gtt aga aat tta aca act aca aag	576
Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys	
180 185 190	
gag atg cca gaa ctt att gaa tta aat gag gtt tta gag gat tta aga	624
Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg	
195 200 205	
att tct ttg gat gat ttg ata gat ata gcc ata ttt atg gga act gac	672
Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp	
210 215 220	

tat aat cca gga gga gtt aaa gga ata gga ttt aaa agg gct tat gaa	720
Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu	
225 230 235 240	
ttg gtt aga agt ggt gta gct aag gat gtt ttg aaa aaa gag gtt gaa	768
Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu	
245 250 255	
tac tac gat gag att aag agg ata ttt aaa gag cca aag gtt acc gat	816
Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp	
260 265 270	
aac tat tca tta agc cta aaa ttg cca gat aaa gag gga att ata aaa	864
Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys	
275 280 285	
ttc tta gtt gat gaa aat gac ttt aat tat gat agg gtt aaa aag cat	912
Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His	
290 295 300	
gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca	960
Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr	
305 310 315 320	
tta gat gca tgg ttt aaa taa	981
Leu Asp Ala Trp Phe Lys	
325	

<210> 75

<211> 326

<212> PRT

<213> Artificial Sequence

<400> 75

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
85 90 95

Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
 100 105 110

Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
 115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
 130 135 140

Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
 165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
 210 215 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
 225 230 235 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
 245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320

Leu Asp Ala Trp Phe Lys
 325

<210> 76
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 76
 gaggtgatac catgggtgtc c 21
 <210> 77
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 77
 gaaactctgc agcgcgtcag 20
 <210> 78
 <211> 1023
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> CDS
 <222> (1)..(1020)
 <400> 78
 atg ggt gtc cca att ggt gag att ata cca aga aaa gaa att gag tta 48
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc 96
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg 144
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45

gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg 50 55 60	192
aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp 65 70 75 80	240
gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu 85 90 95	288
gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly 100 105 110	336
gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn 115 120 125	384
gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile 130 135 140	432
cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met 145 150 155 160	480
gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser 165 170 175	528
cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly 180 185 190	576
aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu 195 200 205	624
ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu 210 215 220	672
aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly 225 230 235 240	720
gga ata aag ggc ata ggc ctt aaa aaa gct tta gag att gtt aga cac Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His 245 250 255	768
tca aaa gat ccg cta gca aag ttc caa aag caa agc gat gtg gat tta Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu 260 265 270	816
tat gca ata aaa gag ttc ttc cta aac cca cca gtc aca gat aac tac Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr 275 280 285	864

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu 290 295 300	912
tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu 305 310 315 320	960
agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser 325 330 335	1008
tgg ttc aag aga taa Trp Phe Lys Arg 340	1023
<210> 79	
<211> 340	
<212> PRT	
<213> Artificial Sequence	
<400> 79	
Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu 1 5 10 15	
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile 20 25 30	
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met 35 40 45	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg 50 55 60	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp 65 70 75 80	
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu 85 90 95	
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly 100 105 110	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn 115 120 125	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile 130 135 140	

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
 145 150 155 160
 Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175
 Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190
 Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205
 Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80
 gataccatgg gtgtcccaat tggtg 25
 <210> 81
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 81
 tcgacgtcga cttatctctt gaaccaactt tcaaggg 37
 <210> 82
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 82
 agcgagggag aggccaagc 20
 <210> 83
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 83
 gcctatgccc tttattcctc c 21
 <210> 84
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 84
 tggtcgctgt ctcgctgaaa gcgagacagc gtg 33

<210> 85
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 85
 tgctctctgg tcgctgtctg aaagacagcg 30
 <210> 86
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <400> 86
 agaaaggaag ggaagaaagc gaaagg 26
 <210> 87
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye

<220>
 <221> modified_base
 <222> (27)..(27)
 <223> The residue at this position is a dideoxycytidine.
 <400> 87
 agaaaggaag ggaagaaagc gaaaggc 27
 <210> 88
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (24)..(24)
 <223> The residue at this position is a dideoxycytidine.
 <400> 88
 gccggcggaac gtggcgagaa aggc 24
 <210> 89
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label

<220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <220>
 <221> modified_base
 <222> (27)..(27)
 <223> The residue at this position is a dideoxycytidine.
 <400> 89
 agaaaggaag ggaagaaagc gaaaggc 27
 <210> 90
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 90
 aaaattcctt tctctttgcc ctttgcttcc 30
 <210> 91
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 91
 ggaaagccgg cgaacgtggc gagaaa 26
 <210> 92
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 92
 ggaaagccgg cgaacgtggc gaga 24
 <210> 93
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing Cy3
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <400> 93
 agaaaggaag ggaagaaagc gaaaggt 27
 <210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing Cy3

<220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions are amine-T.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <400> 94
 ttccagagcc taatttgcca gta 23
 <210> 95
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> The residue at this position has a 5' TET-label.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <400> 95
 ttccagagcc taatttgcca gta 23
 <210> 96
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 96	
cttaccaacg ctaacgagcg tcttg	25
<210> 97	
<211> 43	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 97	
cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca ata	43
<210> 98	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 98	
tattgggcgc catggtggtt ttt	23
<210> 99	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<220>	
<221> misc_difference	
<222> (10)..(10)	
<223> The residue at this position is a 5-nitroindole.	
<220>	
<221> misc_difference	
<222> (16)..(16)	
<223> The residue at this position is a 5-nitroindole.	

<400> 99
 tattgggcgn cagggngggtt ttt 23

 <210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residue at this position is a 5-nitroindole.
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 5-nitroindole.

 <400> 100
 tattgggcgn catggngggtt ttt 23

 <210> 101
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 3-nitropyrrole group.

 <400> 101
 tattgggcgc cagggngggtt ttt 23

<210> 102
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 3-nitropyrrole group.
 <400> 102
 tattgggcgc catggngggtt ttt 23
 <210> 103
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyctosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)

<220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(10)
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <400> 103
 ctgaatataa acttggtgga gttggagctg gtgccgtagg caagagtgcc ttgacg 56
 <210> 104
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyctosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>
 <221> misc_difference
 <222> (9)..(10)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <400> 104
 ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg 56
 <210> 105
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(4)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>
 <221> misc_difference
 <222> (5)..(6)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(8)
 <223> The residues at these positions are a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <400> 105
 gctcaaggca ctcttgcccta cga 23
 <210> 106
 <211> 8
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer bearing a Cy3 amidite label
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions have an amino group added.
 <400> 106
 ttcaccag 8

<210> 107
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(4)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (5)..(6)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiophosphoryl)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiophosphoryl)
 <400> 107
 ctccaactac cacaagttta tattcag 27
 <210> 108
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 108
 cgagagacca cgct 14
 <210> 109
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (14)..(14)
 <223> The residue at this position contains an abasic ribose.
 <400> 109
 cgagagacca cgct 14

<210> 110
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (14)..(14)
 <223> The residue at this position contains an abasic ribose with a 3' phosphate group
 <400> 110
 cgagagacca cgct 14
 <210> 111
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (15)..(15)
 <223> The residue at this position contains a 3' phosphate group.
 <400> 111
 cgagagacca cgctg 15
 <210> 112
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(4)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (5)..(5)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon
 ophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)

<220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi
 omonophosphate)
 <400> 112
 gtaatcttac caacgctaac gagcgtcttg 30
 <210> 113
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(2)
 <223> The residues at these positions are a 2'deoxyctosine 5'-O-(1-Thi
 omonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th
 iomonophosphate)

<220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon
 ophosphate)
 <400> 113
 cctaatttgc cagttacaaa ataaacagcc c 31
 <210> 114
 <211> 8
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions have an amino group added.
 <400> 114
 ttccagag 8

<210> 115
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 115
 ttttccagag cctaataaaa ttaggctctg gaaagacgct cgtg 44
 <210> 116
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 116
 aacgagcgtc tttg 14
 <210> 117
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 117
 aacgagcgtc attg 14
 <210> 118
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 118
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg 50

<210>	119	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	119	
	ttttccagag cctaag	17
<210>	120	
<211>	13	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<220>		
<221>	misc_difference	
<222>	(1)..(1)	
<223>	The residue at this position has a TET label.	
<400>	120	
	ccggtcgtcc tgg	13
<210>	121	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	121	
	caattccggt gtactcaccg gttcc	25
<210>	122	
<211>	16	
<212>	DNA	

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position has a TET label.
 <400> 122
 ccggtcgtcc tggcaa 16
 <210> 123
 <211> 47
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 123
 tgttttgacc tccatagaag accctatagt gagtcgtatt aatttcg 47
 <210> 124
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 124
 cgaaattaat acgactcact ata 23
 <210> 125
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 125
 cgaaattaat acgactcact ataccagaa 30

<210> 126	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 126	
cgaaattaat acgact	16
<210> 127	
<211> 13	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 127	
cgaaattaat acg	13
<210> 128	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 128	
cgaaattaat ac	12
<210> 129	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
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<400> 129	
cactataggg tcttctatgg aggtc	25

<210> 130	
<211> 28	
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actcactata gggctcttcta tggaggtc	28
<210> 131	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
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<223> Synthetic	
<400> 131	
gactcactat aggggtcttct atggaggtc	29
<210> 132	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
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cgaaattaat acgcagtatg ttagcaaacg	30
<210> 133	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
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gaactggcat gattaagact ccttattacc	30

<210> 134

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 134

gaactggcat gattaagact ccttattaa

29

<210> 135

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 135

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20 25 30
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65 70 75 80
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
85 90 95
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
100 105 110
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
115 120 125
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
130 135 140
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
 210 215 220
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
 225 230 235 240
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
 245 250 255
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320
 Leu Asp Ala Trp Phe Lys
 325

<210> 136

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 136

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
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 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95

<400> 137

Met	Gly	Ile	Gln	Gly	Leu	Ala	Lys	Leu	Ile	Ala	Asp	Val	Ala	Pro	Ser	1	5	10	15
Ala	Ile	Arg	Glu	Asn	Asp	Ile	Lys	Ser	Tyr	Phe	Gly	Arg	Lys	Val	Ala	20	25	30	
Ile	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Ala	Val	Arg	Gln	35	40	45	
Gly	Gly	Asp	Val	Leu	Gln	Asn	Glu	Glu	Gly	Glu	Thr	Thr	Ser	His	Leu	50	55	60	
Met	Gly	Met	Phe	Tyr	Arg	Thr	Ile	Arg	Met	Met	Glu	Asn	Gly	Ile	Lys	65	70	75	80
Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	85	90	95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	100	105	110	
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys	115	120	125	
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu	130	135	140	
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	145	150	155	160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	165	170	175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	180	185	190	
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	195	200	205	
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	210	215	220	
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	225	230	235	240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile	245	250	255	
Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu	260	265	270	
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	275	280	285	
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	290	295	300	
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg	305	310	315	320

Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser
 195 200 205
 Arg Val Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu
 210 215 220
 Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly Ile Gly
 225 230 235 240
 Ala Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile Glu Glu
 245 250 255
 Ile Val Arg Arg Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp
 260 265 270
 Leu His Lys Glu Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp
 275 280 285
 Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu
 290 295 300
 Val Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg Ile Arg
 305 310 315 320
 Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly
 325 330 335
 Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys
 340 345 350
 Arg Lys Glu Pro Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr
 355 360 365
 Gly Gly Ala Gly Lys Phe Arg Arg Gly Lys
 370 375

<210> 139

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

Met Gly Ile Lys Gly Leu Asn Ala Ile Ile Ser Glu His Val Pro Ser
 1 5 10 15
 Ala Ile Arg Lys Ser Asp Ile Lys Ser Phe Phe Gly Arg Lys Val Ala
 20 25 30
 Ile Asp Ala Ser Met Ser Leu Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35 40 45
 Gln Asp Gly Gly Gln Leu Thr Asn Glu Ala Gly Glu Thr Thr Ser His
 50 55 60

Leu Met Gly Met Phe Tyr Arg Thr Leu Arg Met Ile Asp Asn Gly Ile
 65 70 75 80
 Lys Pro Cys Tyr Val Phe Asp Gly Lys Pro Pro Asp Leu Lys Ser His
 85 90 95
 Glu Leu Thr Lys Arg Ser Ser Arg Arg Val Glu Thr Glu Lys Lys Leu
 100 105 110
 Ala Glu Ala Thr Thr Glu Leu Glu Lys Met Lys Gln Glu Arg Arg Leu
 115 120 125
 Val Lys Val Ser Lys Glu His Asn Glu Glu Ala Gln Lys Leu Leu Gly
 130 135 140
 Leu Met Gly Ile Pro Tyr Ile Ile Ala Pro Thr Glu Ala Glu Ala Gln
 145 150 155 160
 Cys Ala Glu Leu Ala Lys Lys Gly Lys Val Tyr Ala Ala Ala Ser Glu
 165 170 175
 Asp Met Asp Thr Leu Cys Tyr Arg Thr Pro Phe Leu Leu Arg His Leu
 180 185 190
 Thr Phe Ser Glu Ala Lys Lys Glu Pro Ile His Glu Ile Asp Thr Glu
 195 200 205
 Leu Val Leu Arg Gly Leu Asp Leu Thr Ile Glu Gln Phe Val Asp Leu
 210 215 220
 Cys Ile Met Leu Gly Cys Asp Tyr Cys Glu Ser Ile Arg Gly Val Gly
 225 230 235 240
 Pro Val Thr Ala Leu Lys Leu Ile Lys Thr His Gly Ser Ile Glu Lys
 245 250 255
 Ile Val Glu Phe Ile Glu Ser Gly Glu Ser Asn Asn Thr Lys Trp Lys
 260 265 270
 Ile Pro Glu Asp Trp Pro Tyr Lys Gln Ala Arg Met Leu Phe Leu Asp
 275 280 285
 Pro Glu Val Ile Asp Gly Asn Glu Ile Asn Leu Lys Trp Ser Pro Pro
 290 295 300
 Lys Glu Lys Glu Leu Ile Glu Tyr Leu Cys Asp Asp Lys Lys Phe Ser
 305 310 315 320
 Glu Glu Arg Val Lys Ser Gly Ile Ser Arg Leu Lys Lys Gly Leu Lys
 325 330 335
 Ser Gly Ile Gln Gly Arg Leu Asp Gly Phe Phe Gln Val Val Pro Lys
 340 345 350
 Thr Lys Glu Gln Leu Ala Ala Ala Lys Arg Ala Gln Glu Asn Lys
 355 360 365
 Lys Leu Asn Lys Asn Lys Asn Lys Val Thr Lys Gly Arg Arg
 370 375 380

<210> 140

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

Met	Gly	Val	His	Ser	Phe	Trp	Asp	Ile	Ala	Gly	Pro	Thr	Ala	Arg	Pro	
1				5					10					15		
Val	Arg	Leu	Glu	Ser	Leu	Glu	Asp	Lys	Arg	Met	Ala	Val	Asp	Ala	Ser	
		20						25					30			
Ile	Trp	Ile	Tyr	Gln	Phe	Leu	Lys	Ala	Val	Arg	Asp	Gln	Glu	Gly	Asn	
		35					40					45				
Ala	Val	Lys	Asn	Ser	His	Ile	Thr	Gly	Phe	Phe	Arg	Arg	Ile	Cys	Lys	
		50				55					60					
Leu	Leu	Tyr	Phe	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	Gly	Gly	Val	
65					70					75					80	
Pro	Val	Leu	Lys	Arg	Glu	Thr	Ile	Arg	Gln	Arg	Lys	Glu	Arg	Arg	Gln	
				85					90					95		
Gly	Lys	Arg	Glu	Ser	Ala	Lys	Ser	Thr	Ala	Arg	Lys	Leu	Leu	Ala	Leu	
			100					105					110			
Gln	Leu	Gln	Asn	Gly	Ser	Asn	Asp	Asn	Glu	Val	Thr	Met	Asp	Met	Ile	
		115					120					125				
Lys	Glu	Val	Gln	Glu	Leu	Leu	Ser	Arg	Phe	Gly	Ile	Pro	Tyr	Ile	Thr	
	130					135					140					
Ala	Pro	Met	Glu	Ala	Glu	Ala	Gln	Cys	Ala	Glu	Leu	Leu	Gln	Leu	Asn	
145					150					155					160	
Leu	Val	Asp	Gly	Ile	Ile	Thr	Asp	Asp	Ser	Asp	Val	Phe	Leu	Phe	Gly	
				165					170					175		
Gly	Thr	Lys	Ile	Tyr	Lys	Asn	Met	Phe	His	Glu	Lys	Asn	Tyr	Val	Glu	
			180					185					190			
Phe	Tyr	Asp	Ala	Glu	Ser	Ile	Leu	Lys	Leu	Leu	Gly	Leu	Asp	Arg	Lys	
		195					200					205				
Asn	Met	Ile	Glu	Leu	Ala	Gln	Leu	Leu	Gly	Ser	Asp	Tyr	Thr	Asn	Gly	
	210					215					220					
Leu	Lys	Gly	Met	Gly	Pro	Val	Ser	Ser	Ile	Glu	Val	Ile	Ala	Glu	Phe	
225					230					235					240	
Gly	Asn	Leu	Lys	Asn	Phe	Lys	Asp	Trp	Tyr	Asn	Asn	Gly	Gln	Phe	Asp	
				245					250					255		

Asn Phe Leu Ala Ser Leu Thr Pro Lys Thr Asn Ser Ser Ser Ile Ser
 450 455 460
 Ile Glu Asn Leu Pro Arg Lys Thr Lys Leu Ser Thr Ser Leu Leu Lys
 465 470 475 480
 Lys Pro Ser Lys Arg Arg Arg Lys
 485
 <210> 142
 <211> 550
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 142
 Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Gln
 1 5 10 15
 Val Ser Pro Glu Ala Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser
 20 25 30
 Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Arg His Gly Asn
 35 40 45
 Ser Ile Glu Asn Pro His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
 50 55 60
 Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala
 65 70 75 80
 Pro Leu Leu Lys Lys Gln Thr Leu Val Lys Arg Arg Gln Arg Lys Asp
 85 90 95
 Leu Ala Ser Ser Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr
 100 105 110
 Phe Leu Lys Arg Gln Ala Ile Lys Thr Glu Arg Ile Ala Ala Thr Val
 115 120 125
 Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly
 130 135 140
 Ile Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile
 145 150 155 160
 Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
 165 170 175
 Ile Trp Leu Phe Gly Ala Arg His Val Tyr Arg Asn Phe Phe Asn Lys
 180 185 190
 Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe His Asn Gln Leu
 195 200 205

Gly Leu Asp Arg Asn Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
 210 215 220
 Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Cys Val Thr Ala Met Glu
 225 230 235 240
 Ile Leu Asn Glu Phe Pro Gly His Gly Leu Glu Pro Leu Leu Lys Phe
 245 250 255
 Ser Glu Trp Trp His Glu Ala Gln Lys Asn Pro Lys Ile Arg Pro Asn
 260 265 270
 Pro His Asp Thr Lys Val Lys Lys Lys Leu Arg Thr Leu Gln Leu Thr
 275 280 285
 Pro Gly Phe Pro Asn Pro Ala Val Ala Glu Ala Tyr Leu Lys Pro Val
 290 295 300
 Val Asp Asp Ser Lys Gly Ser Phe Leu Trp Gly Lys Pro Asp Leu Asp
 305 310 315 320
 Lys Ile Arg Glu Phe Cys Gln Arg Tyr Phe Gly Trp Asn Arg Thr Lys
 325 330 335
 Thr Asp Glu Ser Leu Phe Pro Val Leu Lys Gln Leu Asp Ala Gln Gln
 340 345 350
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Ala Gln Gln Glu Lys
 355 360 365
 Glu Asp Ala Lys Arg Ile Lys Ser Gln Arg Leu Asn Arg Ala Val Thr
 370 375 380
 Cys Met Leu Arg Lys Glu Lys Glu Ala Ala Ala Ser Glu Ile Glu Ala
 385 390 395 400
 Val Ser Val Ala Met Glu Lys Glu Phe Glu Leu Leu Asp Lys Ala Lys
 405 410 415
 Arg Lys Thr Gln Lys Arg Gly Ile Thr Asn Thr Leu Glu Glu Ser Ser
 420 425 430
 Ser Leu Lys Arg Lys Arg Leu Ser Asp Ser Lys Arg Lys Asn Thr Cys
 435 440 445
 Gly Gly Phe Leu Gly Glu Thr Cys Leu Ser Glu Ser Ser Asp Gly Ser
 450 455 460
 Ser Ser Glu His Ala Glu Ser Ser Ser Leu Met Asn Val Gln Arg Arg
 465 470 475 480
 Thr Ala Ala Lys Glu Pro Lys Thr Ser Ala Ser Asp Ser Gln Asn Ser
 485 490 495
 Val Lys Glu Ala Pro Val Lys Asn Gly Gly Ala Thr Thr Ser Ser Ser
 500 505 510

Ser Asp Ser Asp Asp Asp Gly Gly Lys Glu Lys Met Val Leu Val Thr
 515 520
 Ala Arg Ser Val Phe Gly Lys Lys Arg Arg Lys Leu Arg Arg Ala Arg
 530 535 540
 Gly Arg Lys Arg Lys Thr
 545 550
 <210> 143
 <211> 543
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 143
 Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly His Arg
 1 5 10 15
 Val Ser Pro Glu Ala Leu Glu Gly Lys Val Leu Ala Val Asp Ile Ser
 20 25 30
 Ile Trp Leu Asn Gln Ala Leu Lys Gly Val Arg Asp Ser His Gly Asn
 35 40 45
 Val Ile Glu Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
 50 55 60
 Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Asp Ala
 65 70 75 80
 Pro Leu Leu Lys Lys Gln Thr Leu Ala Lys Arg Arg Gln Arg Lys Asp
 85 90 95
 Ser Ala Ser Ile Asp Ser Arg Lys Thr Thr Glu Lys Leu Leu Lys Thr
 100 105 110
 Phe Leu Lys Arg Gln Ala Leu Lys Thr Asp Arg Ile Ala Ala Ser Val
 115 120 125
 Thr Gly Gln Met Phe Leu Glu Ser Gln Glu Leu Leu Arg Leu Phe Gly
 130 135 140
 Val Pro Tyr Ile Gln Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Val
 145 150 155 160
 Leu Asp Leu Ser Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
 165 170 175
 Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Asn Lys
 180 185 190
 Asn Lys Phe Val Glu Tyr Tyr Gln Tyr Val Asp Phe Tyr Ser Gln Leu
 195 200 205

Gly	Leu	Asp	Arg	Asn	Lys	Leu	Ile	Asn	Leu	Ala	Tyr	Leu	Leu	Gly	Ser	210	215	220
Asp	Tyr	Thr	Glu	Gly	Ile	Pro	Thr	Val	Gly	Cys	Val	Thr	Ala	Met	Glu	225	230	235
Ile	Leu	Asn	Glu	Phe	Pro	Gly	Arg	Gly	Leu	Asp	Pro	Leu	Leu	Lys	Phe	245	250	255
Ser	Glu	Trp	Trp	His	Glu	Ala	Gln	Asn	Asn	Lys	Lys	Val	Ala	Glu	Asn	260	265	270
Pro	Tyr	Asp	Thr	Lys	Val	Lys	Lys	Lys	Leu	Arg	Lys	Leu	Gln	Leu	Thr	275	280	285
Pro	Gly	Phe	Pro	Asn	Pro	Ala	Val	Ala	Asp	Ala	Tyr	Leu	Arg	Pro	Val	290	295	300
Val	Asp	Asp	Ser	Arg	Gly	Ser	Phe	Leu	Trp	Gly	Lys	Pro	Asp	Val	Asp	305	310	315
Lys	Ile	Arg	Glu	Phe	Cys	Gln	Arg	Tyr	Phe	Gly	Trp	Asn	Arg	Met	Lys	325	330	335
Thr	Asp	Glu	Ser	Leu	Tyr	Pro	Val	Leu	Lys	His	Leu	Asn	Ala	His	Gln	340	345	350
Thr	Gln	Leu	Arg	Ile	Asp	Ser	Phe	Phe	Arg	Leu	Ala	Gln	Gln	Glu	Lys	355	360	365
Gln	Asp	Ala	Lys	Leu	Ile	Lys	Ser	His	Arg	Leu	Ser	Arg	Ala	Val	Thr	370	375	380
Cys	Met	Leu	Arg	Lys	Glu	Arg	Glu	Glu	Lys	Ala	Pro	Glu	Leu	Thr	Lys	385	390	395
Val	Thr	Glu	Ala	Met	Glu	Lys	Glu	Phe	Glu	Leu	Leu	Asp	Asp	Ala	Lys	405	410	415
Gly	Lys	Thr	Gln	Lys	Arg	Glu	Leu	Pro	Tyr	Lys	Lys	Glu	Thr	Ser	Val	420	425	430
Pro	Lys	Arg	Arg	Arg	Pro	Ser	Gly	Asn	Gly	Gly	Phe	Leu	Gly	Asp	Pro	435	440	445
Tyr	Cys	Ser	Glu	Ser	Pro	Gln	Glu	Ser	Ser	Cys	Glu	Asp	Gly	Glu	Gly	450	455	460
Ser	Ser	Val	Met	Ser	Ala	Arg	Gln	Arg	Ser	Ala	Ala	Glu	Ser	Ser	Lys	465	470	475
Ile	Gly	Cys	Ser	Asp	Val	Pro	Asp	Leu	Val	Arg	Asp	Ser	Pro	His	Gly	485	490	495
Arg	Gln	Gly	Cys	Val	Ser	Thr	Ser	Ser	Ser	Asp	Ser	Glu	Asp	Gly	Glu	500	505	510
Asp	Lys	Ala	Lys	Thr	Val	Leu	Val	Thr	Ala	Arg	Pro	Val	Phe	Gly	Lys	515	520	525
Lys	Arg	Arg	Lys	Leu	Lys	Ser	Met	Lys	Arg	Arg	Lys	Lys	Lys	Thr		530	535	540

<210> 144

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 144

Met Gly Val Gln Gly Leu Trp Lys Leu Leu Glu Cys Ser Gly Arg Pro
1 5 10 15
Ile Asn Pro Gly Thr Leu Glu Gly Lys Ile Leu Ala Val Asp Ile Ser
20 25 30
Ile Trp Leu Asn Gln Ala Val Lys Gly Ala Arg Asp Arg Gln Gly Asn
35 40 45
Ala Ile Gln Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
50 55 60
Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Glu Ala
65 70 75 80
Pro Leu Leu Lys Arg Gln Thr Leu Ala Lys Arg Arg Gln Arg Thr Asp
85 90 95
Lys Ala Ser Asn Asp Ala Arg Lys Thr Asn Glu Lys Leu Leu Arg Thr
100 105 110
Phe Leu Lys Arg Gln Ala Ile Lys Ala Glu Arg Ile Ala Ala Thr Val
115 120 125
Thr Gly Gln Met Cys Leu Glu Ser Gln Glu Leu Leu Gln Leu Phe Gly
130 135 140
Ile Pro Tyr Ile Val Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile
145 150 155 160
Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
165 170 175
Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Ser Gln
180 185 190
Asn Lys His Val Glu Tyr Tyr Gln Tyr Ala Asp Ile His Asn Gln Leu
195 200 205
Gly Leu Asp Arg Ser Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
210 215 220
Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Tyr Val Ser Ala Met Glu
225 230 235 240
Ile Leu Asn Glu Phe Pro Gly Gln Gly Leu Glu Pro Leu Val Lys Phe
245 250 255

Lys Glu Trp Trp Ser Glu Ala Gln Lys Asp Lys Lys Met Arg Pro Asn
 260 265 270
 Pro Asn Asp Thr Lys Val Lys Lys Lys Leu Arg Leu Leu Asp Leu Gln
 275 280 285
 Gln Ser Phe Pro Asn Pro Ala Val Ala Ser Ala Tyr Leu Lys Pro Val
 290 295 300
 Val Asp Glu Ser Lys Ser Ala Phe Ser Trp Gly Arg Pro Asp Leu Glu
 305 310 315 320
 Gln Ile Arg Glu Phe Cys Glu Ser Arg Phe Gly Trp Tyr Arg Leu Lys
 325 330 335
 Thr Asp Glu Val Leu Leu Pro Val Leu Lys Gln Leu Asn Ala Gln Gln
 340 345 350
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Glu Gln His Glu Ala
 355 360 365
 Ala Gly Leu Lys Ser Gln Arg Leu Arg Arg Ala Val Thr Cys Met Lys
 370 375 380
 Arg Lys Glu Arg Asp Val Glu Ala Glu Glu Val Glu Ala Ala Val Ala
 385 390 395 400
 Val Met Glu Arg Glu Cys Thr Asn Gln Arg Lys Gly Gln Lys Thr Asn
 405 410 415
 Thr Lys Ser Gln Gly Thr Lys Arg Arg Lys Pro Thr Glu Cys Ser Gln
 420 425 430
 Glu Asp Gln Asp Pro Gly Gly Gly Phe Ile Gly Ile Glu Leu Lys Thr
 435 440 445
 Leu Ser Ser Lys Ala Tyr Ser Ser Asp Gly Ser Ser Ser Asp Ala Glu
 450 455 460
 Asp Leu Pro Ser Gly Leu Ile Asp Lys Gln Ser Gln Ser Gly Ile Val
 465 470 475 480
 Gly Arg Gln Lys Ala Ser Asn Lys Val Glu Ser Ser Ser Ser Ser Asp
 485 490 495
 Asp Glu Asp Arg Thr Val Met Val Thr Ala Lys Pro Val Phe Gln Gly
 500 505 510
 Lys Lys Thr Lys Ser Lys Thr Met Lys Glu Thr Val Lys Arg Lys
 515 520 525
 <210> 145
 <211> 434
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 145

Met Thr Ile Asn Gly Ile Trp Glu Trp Ala Asn His Val Val Arg Lys
1 5 10 15
Val Pro Asn Glu Thr Met Arg Asp Lys Thr Leu Ser Ile Asp Gly His
20 25 30
Ile Trp Leu Tyr Glu Ser Leu Lys Gly Cys Glu Ala His His Gln Gln
35 40 45
Thr Pro Asn Ser Tyr Leu Val Thr Phe Phe Thr Arg Ile Gln Arg Leu
50 55 60
Leu Glu Leu Lys Ile Ile Pro Ile Val Val Phe Asp Asn Ile Asn Ala
65 70 75 80
Ser Ser Ser Ala His Glu Ser Lys Asp Gln Asn Glu Phe Val Pro Arg
85 90 95
Lys Arg Arg Ser Phe Gly Asp Ser Pro Phe Thr Asn Leu Val Asp His
100 105 110
Val Tyr Lys Thr Asn Ala Leu Leu Thr Glu Leu Gly Ile Lys Val Ile
115 120 125
Ile Ala Pro Gly Asp Gly Glu Ala Gln Cys Ala Arg Leu Glu Asp Leu
130 135 140
Gly Val Thr Ser Gly Cys Ile Thr Thr Asp Phe Asp Tyr Phe Leu Phe
145 150 155 160
Gly Gly Lys Asn Leu Tyr Arg Phe Asp Phe Thr Ala Gly Thr Ser Ser
165 170 175
Thr Ala Cys Leu His Asp Ile Met His Leu Ser Leu Gly Arg Met Phe
180 185 190
Met Glu Lys Lys Val Ser Arg Pro His Leu Ile Ser Thr Ala Ile Leu
195 200 205
Leu Gly Cys Asp Tyr Phe Gln Arg Gly Val Gln Asn Ile Gly Ile Val
210 215 220
Ser Val Phe Asp Ile Leu Gly Glu Phe Gly Asp Asp Gly Asn Glu Glu
225 230 235 240
Ile Asp Pro His Val Ile Leu Asp Arg Phe Ala Ser Tyr Val Arg Glu
245 250 255
Glu Ile Pro Ala Arg Ser Glu Asp Thr Gln Arg Lys Leu Arg Leu Arg
260 265 270
Arg Lys Lys Tyr Asn Phe Pro Val Gly Phe Pro Asn Cys Asp Ala Val
275 280 285

His Asn Ala Ile Thr Met Tyr Leu Arg Pro Pro Val Ser Ser Glu Ile
 290 295 300
 Pro Lys Ile Ile Pro Arg Ala Ala Asn Phe Gln Gln Val Ala Glu Ile
 305 310 315 320
 Met Met Lys Glu Cys Gly Trp Pro Ala Thr Arg Thr Gln Lys Glu Leu
 325 330 335
 Ala Leu Ser Ile Arg Arg Lys Val His Leu Thr Thr Thr Val Ala Gln
 340 345 350
 Thr Arg Ile Pro Asp Phe Phe Ala Ala Thr Lys Ser Lys Asn Phe Thr
 355 360 365
 Pro Ile Val Glu Pro Cys Glu Ser Leu Glu Asp Tyr Ile Ser Ala Asn
 370 375 380
 Asn Thr Trp Met Arg Lys Arg Lys Arg Ser Glu Ser Pro Gln Ile Leu
 385 390 395 400
 Gln His His Ala Lys Arg Gln Val Pro Asp Arg Lys Arg Ser Val Lys
 405 410 415
 Ile Arg Ala Phe Lys Pro Tyr Pro Thr Asp Val Ile Glu Leu Gly Asp
 420 425 430
 Ser Asp

<210> 146

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146

tactgactca ctatagggtc ttctatggag gtc

33

<210> 147

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 147	
ttttttttta attaggctct ggaagacgct gaaagcgtct tg	42
<210> 148	
<211> 38	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 148	
ttttttttta attaggctct ggaagacgga acgtcttg	38
<210> 149	
<211> 34	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 149	
ttttttttta attaggctct ggaagagaat cttg	34
<210> 150	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 150	
ttttttttta attaggctct ggaaggaact tg	32
<210> 151	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	

<400> 151	
tttttttttta attaggctct ggaag	25
<210> 152	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<220>	
<221> misc_difference	
<222> (1)..(1)	
<223> The residue at this position has a TET label.	
<400> 152	
attagaaagg aagggaagaa agcgaa	26
<210> 153	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 153	
acggggaaag ccggcgaacg tggcgagaaa	30
<210> 154	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 154	
tgacggggaa agccggcgaa cgtggcgaga	30

<210> 155
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 155
 cttgacgggg aaagccggcg aacgtggcga 30
 <210> 156
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 156
 gcttgacggg gaaagccggc gaacgtggcg 30
 <210> 157
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 157
 agaaaggaag ggaagaaa 18
 <210> 158
 <211> 45
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 158
 tggaggtcaa aacatcgata agtcgaagaa aggaagggaa gaaat 45
 <210> 159
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 159
 tgttttgacc tcca 14
 <210> 160
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 160
 acacagtgtc ctcccgtcc tcctgagcaa 30
 <210> 161
 <211> 18
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 161
 tttccctcct cctcttcc 18
 <210> 162
 <211> 54
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 162
 atgaggaaga ggaggagggt gctcaggagg agcgggagga cactgtgtct gtca 54
 <210> 163
 <211> 53
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 163
 ttcgctttct tcccttcctt tctcgccacg ttcgccggt ttccccgtca agc 53
 <210> 164
 <211> 1011
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

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<400> 164
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtggt tgtattcgac 240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttaagtac 420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaatgctc 600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
aatcctcctg tgactgacga ctacagaata gaggtcaggg agcctgactt tgagaaggcc 900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttctg a 1011

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<210> 165

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20           25           30
Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35           40           45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50           55           60

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Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	130	135	140	
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	165	170		175
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	180	185	190	
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	195	200	205	
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	210	215	220	
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val	225	230	235	240
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	245	250	255	
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val	260	265	270	
Glu	Glu	Ile	Arg	Asn	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asp	Tyr	275	280	285	
Arg	Ile	Glu	Phe	Arg	Glu	Pro	Asp	Phe	Glu	Lys	Ala	Ile	Glu	Phe	Leu	290	295	300	
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu	305	310	315	320
Lys	Leu	Lys	Ala	Leu	Lys	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Arg	Trp	Phe	325	330	335	

<210> 166

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166 ccgtcaacat ttaccatggg tgcgga	26
<210> 167	
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<400> 167 ccgccacctc gtagtcgaca tccttttcgt g	31
<210> 168	
<211> 20	
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<400> 168 ggcgaccaca cccgtcctgt	20
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<213> Artificial Sequence	
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<400> 169 ccacgatgcg tccggcgtag	20
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<211> 29	
<212> DNA	
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<220>
 <221> modified_base
 <222> (29)..(29)
 <223> The residue at this position is a 3' amine.
 <400> 170
 aacgaggcgc acccacccaa ggcacagcn 29
 <210> 171
 <211> 26
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 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 171
 acgggtcaat gtccatgccc caaaga 26
 <210> 172
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(27)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (28)..(28)
 <223> The residue at this position is a 3' amine.
 <400> 172
 gtctgagatg aaagtgcgcc tcgttaan 28

<210> 173
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 173
 tcttcgcaca ttcatctca gacgga 26
 <210> 174
 <211> 22
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (22)..(22)
 <223> The residue at this position is a 3' amine.
 <400> 174
 gctgtgcctt ggggtgggtgc gn 22
 <210> 175
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>

<221> modified_base
 <222> (29)..(29)
 <223> The residue at this position is a 3' amine.
 <400> 175
 aacgaggcgc acccacccaa ggcacagcn 29
 <210> 176
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 176
 acgggtcaat gtccatgccc caaaga 26
 <210> 177
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(27)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (28)..(28)
 <223> The residue at this position is a 3' amine.
 <400> 177
 gtctgagatg aaagtgcgcc tcgttaan 28

<210> 178
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label

 <400> 178
 tcttcgcaca ttcatctca gac 23

 <210> 179
 <211> 18
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(17)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> The residue at this position is a 3' amine.

 <400> 179
 gctgtgcctt gggtgggn 18

<210> 180
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
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 <221> modified_base
 <222> (1)..(19)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (20)..(20)
 <223> The residue at this position is a 3' amine.

<400> 180
 gctgtgcctt ggggtgggtgn

20

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (22)..(22)
 <223> The residue at this position is a 3' amine.

<400> 181
 gctgtgcctt ggggtgggtgc gn

22

<210> 182
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
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 <221> modified_base
 <222> (1)..(22)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (23)..(23)
 <223> The residue at this position is a 3' amine.
 <400> 182
 gctgtgcctt ggggtgggtgc gcn

23

<210> 183
 <211> 42
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <220>
 <221> modified_base
 <222> (22)..(22)
 <223> The residue at this position indicates 2'-O-methyl sugar.

<220>
 <221> modified_base
 <222> (42)..(42)
 <223> The residue at this position is a 3' amine.
 <400> 183
 gtctgagatg aaagtgctcc cgcacccacc caaggcacag cn 42
 <210> 184
 <211> 18
 <212> DNA
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 <223> Synthetic
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 <222> (1)..(17)
 <223> The residues at these positions are 2'-O-methyl sugars.
 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> The residue at this position is a 3' amine.
 <400> 184
 gctgtgcctt gggtgggn 18
 <210> 185
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
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 <221> misc_difference
 <222> (29)..(29)
 <223> The residue at this position is a 3' primer.

<400> 185
 aacgaggcgc acccacccaa ggcacagcn 29
 <210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 186
 gctgtgcctt ggggtgggtgc g 21
 <210> 187
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.
 <400> 187
 gctgtgcctt ggggtgggtgc n 21
 <210> 188
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (15)..(20)
 <223> The residues at these positions are 2'-O-methyl sugars.

<220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.
 <400> 188
 gctgtgcctt ggggtgggtgc n 21
 <210> 189
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(20)
 <223> The residues at these positions are 2'-O-methyl sugars.
 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.
 <400> 189
 gctgtgcctt ggggtgggtgc n 21
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 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
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 <400> 190
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 <210> 191
 <211> 54
 <212> DNA
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 <223> Synthetic
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 <211> 54
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
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 <210> 193
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 193
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<210> 194
 <211> 56
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 194
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 <210> 195
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> cggtactgcaccaggcgccgct
 <400> 195
 cggtactgca ccaggcggcc gct 23
 <210> 196
 <211> 25
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 196
 ccccggcctg gtacactgcc aggct 25
 <210> 197
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 197
 aacgaggcgc acgcacgtcc tccatgt 27

<210> 198
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (24)..(24)
 <223> The residue at this position is linked to 2-amino deoxyadenosine.
 <400> 198
 gaacgaggcg cacacacgtc ctcttgt 27
 <210> 199
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 199
 aacgaggcg acgcttctgc aggtcatc 28
 <210> 200
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (20)..(20)
 <223> The residue at this position is linked to 2-amino deoxyadenosine.
 <400> 200
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<210> 201
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 201
 cctcgtctcg gttttccgag acgaggggtgc gcctcgttc 39
 <210> 202
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 202
 cccctgggga agagcagaga tatacgtc 28
 <210> 203
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 203
 gggctccaca cggcgactct catt 24

<210> 204
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 204
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 <210> 205
 <211> 39
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 205
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 <210> 206
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 206
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 <210> 207
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 207
 agctgttcgt gttctatgat gatgagagtc gccgtgtgga gccccg 46

<210> 208
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 208
 aacgaacgcg caggccaggt ggagcattt 29
 <210> 209
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 209
 aacgaacgcg cagaccaggt ggagcac 27
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 <211> 40
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 211
 aagcacgcag cacgatcata gaacacgaac agttt 35
 <210> 212
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 212
 aagcacgcag caccatcata gaacacgaac agttt 35
 <210> 213
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 213
 acgcgtctcg gttttccgag acgcgtgtgc tgcgtgcuuu 40
 <210> 214
 <211> 50
 <212> DNA
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 <223> Synthetic
 <400> 214
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<211>	30	
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	caaagaaaag ctgcgtgatg atgaaatcgc	30
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<211>	26	
<212>	DNA	
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	aacgaggcgc acgctcccgc agacac	26
<210>	218	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	Synthetic	
<400>	218	
	aacgaggcgc acactcccgc agacacc	27

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 <212> DNA
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 <223> Synthetic
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 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <210> 221
 <211> 51
 <212> DNA
 <213> Artificial Sequence
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 <400> 221
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 <400> 222
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 223
 aacgaggcgc acgagcctca atgctccc 28
 <210> 224
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 <213> Artificial Sequence
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 <400> 224
 aacgaggcgc acaagcctca atgctccc 28
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 <223> Synthetic

<220>
 <221> misc_feature
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 <210> 226
 <211> 52
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 226
 tgaagtctag agaaagggtt gtacggctga ggtctggaga aatgggcata tg 52
 <210> 227
 <211> 46
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 227
 tttgaaatgt cacagggttc ctaacagcca ctcttccttg gatggg 46
 <210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 228
 agatgcccac ttctccagac ctcagccc 28

<210> 229
 <211> 36
 <212> DNA
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 <223> Synthetic
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 aagcacgcag cacgtacaac cttttctcta gacaaa 36
 <210> 230
 <211> 40
 <212> DNA
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 ctccgtctcg gttttccgag acggaggtgc tgcgtgcuuu 40
 <210> 231
 <211> 25
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 231
 ccatccaggg aagagtggcc tgttt 25

<210> 232
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 232
 aagcacgcag cacaggaacc ctgtgacat 29
 <210> 233
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 <400> 233
 taggttttga ggggcatggg gacgggggttc agcctccagg gtccta 46
 <210> 234
 <211> 46
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 234
 taggttttga ggggcatgag gacgggggttc agcctccagg gtccta 46
 <210> 235
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 <223> Synthetic
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 gaccctggag gctgaacccc gtcca 25

<210> 236
 <211> 28
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 aacgaggcgc acccatcggg gtcaaaac 28
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 aacgaggcgc actcatgccc ctcaaaac 28
 <210> 238
 <211> 56
 <212> DNA
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 aaggacaaaa tacctgtatt cctcgctgt ccagggatct gctcttacag attaga 56
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 <211> 56
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 aaggacaaaa tacctgtatt ccttgctgt ccagggatct gctcttacag attaga 56

<210> 240
 <211> 30
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The residue at this position is linked to a purine.
 <400> 240
 taatctgtaa gagcagatcc ctggacagcc 30
 <210> 241
 <211> 33
 <212> DNA
 <213> Artificial Sequence
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 aacgaggcgc acgaggaata caggtatttt gtc 33
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 <400> 242
 aacgaggcgc acaaggaata caggtatttt gtc 33

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 <211> 24
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 <223> Synthetic
 <400> 243
 ggtaaagggtt ggcaaaaaga taac 24
 <210> 244
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 244
 gcgccgaggt cttggggtgg ttacaag 27
 <210> 245
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 245
 tctcgtctcg gttttccgag actgagacct cggcgcg 37
 <210> 246
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 246
 cacttgcttc aggaccatat ttctctctc 29
 <210> 247
 <211> 33
 <212> DNA
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 <400> 247
 cgcgccgagg acaccttttt tagggtgctt tgt 33
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